

38-21(52806) Sequence Listing\_PCT\_2.ST25.txt  
SEQUENCE LISTING

<110> Monsanto Technology LLC

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Roberts, James K.

<120> Insecticidal Proteins Secreted From Bacillus Species and Uses Therefor

<130> 38-21(52806)PCT

<150> US 60/485,483

<151> 2003-07-07

<160> 33

<170> PatentIn version 3.1

<210> 1

<211> 15

<212> PRT

<213> *Bacillus thuringiensis*

<400> 1

Val Ile Gly Pro Tyr Ala Glu Ser Tyr Ile Asp Arg Val Gln Asp  
1 5 10 15

<210> 2

<211> 45

## 38-21(52806) Sequence Listing\_PCT\_2.ST25.txt

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; tic gene probe encoding SEQ ID NO 1

&lt;400&gt; 2

gtaattggac catatgcaga atcatatatatt gatacgagta caaga

45

&lt;210&gt; 3

&lt;211&gt; 1253

&lt;212&gt; DNA

<213> *Bacillus thuringiensis*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (153)..(1253)

&lt;223&gt;

&lt;400&gt; 3

aattatgatt ttaatattct tatgttattc ctataatata caataaaagc ataattatcc

60

ttcatattat gtttataaaat ttaataaaaat acataaaaat agagtgttat aatatttttg

120

aaagcgttat caagagtgat ggaggataa tt atg aaa aat aga ttt tca aaa  
Met Lys Asn Arg Phe Ser Lys  
1 5gtg gca tta tgc acc gta ccg att tta atg gtt tct aca ttc gcc agt  
Val Ala Leu Cys Thr Val Pro Ile Leu Met Val Ser Thr Phe Ala Ser  
10 15 20

221

tca agc atg tca gct ttt gct gca gaa gcc aaa tca cca gat tta aat  
Ser Ser Met Ser Ala Phe Ala Ala Glu Ala Lys Ser Pro Asp Leu Asn  
25 30 35

269

gta tct caa caa gta ata ggt ccc tat gcc gaa tct tat att gat att  
Val Ser Gln Gln Val Ile Gly Pro Tyr Ala Glu Ser Tyr Ile Asp Ile  
40 45 50 55

317

gtg cag gat aga atg aaa caa agg gat aag gga tca aaa tta act ggt  
Val Gln Asp Arg Met Lys Gln Arg Asp Lys Gly Ser Lys Leu Thr Gly  
60 65 70

365

aaa cca ata aat atg caa gaa caa ata ata gat ggg tgg ttt cta gct  
Lys Pro Ile Asn Met Gln Glu Gln Ile Ile Asp Gly Trp Phe Leu Ala  
75 80 85

413

38-21(52806) Sequence Listing\_PCT\_2.ST25.txt

aga ttt tgg ata ttt aag gat caa aac aat aac cat cag aca aat aga	Arg Phe Trp Ile Phe Lys Asp Gln Asn Asn Asn His Gln Thr Asn Arg	461	
90	95	100	
ttt ata tcc tgg ttt aaa gat aat att gct agt tca aaa ggg tat aat	Phe Ile Ser Trp Phe Lys Asp Asn Ile Ala Ser Ser Lys Gly Tyr Asn	509	
105	110	115	
agt att gcg gag caa atg ggt tta aaa ata gaa gca gaa aac gat atg	Ser Ile Ala Glu Gln Met Gly Leu Lys Ile Glu Ala Glu Asn Asp Met	557	
120	125	130	135
gat gta aca aat ata gat tat aca tct aag aca ggc gat acc att tat	Asp Val Thr Asn Ile Asp Tyr Thr Ser Lys Thr Gly Asp Thr Ile Tyr	605	
140	145	150	
aat ggt att tca gaa ttg aaa aat tat aca gga tca act caa aag atg	Asn Gly Ile Ser Glu Leu Lys Asn Tyr Thr Gly Ser Thr Gln Lys Met	653	
155	160	165	
aaa aca gat agt ttt caa aga gat tat aca aaa tca gaa tct act tca	Lys Thr Asp Ser Phe Gln Arg Asp Tyr Thr Lys Ser Glu Ser Thr Ser	701	
170	175	180	
gta act aat gga tta caa tta gga ttt aaa gtt gct gct aaa gga gta	Val Thr Asn Gly Leu Gln Leu Gly Phe Lys Val Ala Ala Lys Gly Val	749	
185	190	195	
gtt gct ttg gct ggg gca gac ttt gaa acc agt gtt act tat aat cta	Val Ala Leu Ala Gly Ala Asp Phe Glu Thr Ser Val Thr Tyr Asn Leu	797	
200	205	210	215
tca act act aca act gaa aca aat aca ata tca gac aag ttt act gtc	Ser Thr Thr Thr Glu Thr Asn Thr Ile Ser Asp Lys Phe Thr Val	845	
220	225	230	
cca tct caa gaa gtt aca ttg cct cca gga cat aaa gcg ata gtg aaa	Pro Ser Gln Glu Val Thr Leu Pro Pro Gly His Lys Ala Ile Val Lys	893	
235	240	245	
cat gat tta aga aaa atg gtt tat tct ggt act cat cat gat cta aag ggt	His Asp Leu Arg Lys Met Val Tyr Ser Gly Thr His Asp Leu Lys Gly	941	
250	255	260	
gat tta att gtg agt ttt aat gat aaa gag att gta caa aaa ttt att	Asp Leu Ile Val Ser Phe Asn Asp Lys Glu Ile Val Gln Lys Phe Ile	989	
265	270	275	
tat cca aat tat aga gaa att aat tta tct gat atc cgt gaa act atg	Tyr Pro Asn Tyr Arg Glu Ile Asn Leu Ser Asp Ile Arg Glu Thr Met	1037	
280	285	290	295
att gaa att gat gaa tgg aat cat gta aac cct gtg aat ttt tat gaa	Ile Glu Ile Asp Glu Trp Asn His Val Asn Pro Val Asn Phe Tyr Glu	1085	
300	305	310	
tta gtt ggg gtc aaa aat cat ata aaa aat ggt gaa act ttg tat ata	Leu Val Gly Val Lys Asn His Ile Lys Asn Gly Glu Thr Leu Tyr Ile	1133	
315	320	325	
gat act cca gct aaa ttt atg ttt aat ggt gct aat cca tat tat aga	Asp Thr Pro Ala Lys Phe Met Phe Asn Gly Ala Asn Pro Tyr Tyr Arg	1181	
330	335	340	

## 38-21(52806) Sequence Listing\_PCT\_2.ST25.txt

gca aca ttt aca gaa tac gac ggg aat aat aat cct gtt caa aca aag 1229  
 Ala Thr Phe Thr Glu Tyr Asp Gly Asn Asn Asn Pro Val Gln Thr Lys  
 345 350 355

gta tta agt gaa aac ttt aaa ttg 1253  
 Val Leu Ser Glu Asn Phe Lys Leu  
 360 365

<210> 4

<211> 367

<212> PRT

<213> *Bacillus thuringiensis*

<400> 4

Met Lys Asn Arg Phe Ser Lys Val Ala Leu Cys Thr Val Pro Ile Leu  
 1 5 10 15

Met Val Ser Thr Phe Ala Ser Ser Met Ser Ala Phe Ala Ala Glu  
 20 25 30

Ala Lys Ser Pro Asp Leu Asn Val Ser Gln Gln Val Ile Gly Pro Tyr  
 35 40 45

Ala Glu Ser Tyr Ile Asp Ile Val Gln Asp Arg Met Lys Gln Arg Asp  
 50 55 60

Lys Gly Ser Lys Leu Thr Gly Lys Pro Ile Asn Met Gln Glu Gln Ile  
 65 70 75 80

Ile Asp Gly Trp Phe Leu Ala Arg Phe Trp Ile Phe Lys Asp Gln Asn  
 85 90 95

Asn Asn His Gln Thr Asn Arg Phe Ile Ser Trp Phe Lys Asp Asn Ile  
 100 105 110

Ala Ser Ser Lys Gly Tyr Asn Ser Ile Ala Glu Gln Met Gly Leu Lys  
 115 120 125

Ile Glu Ala Glu Asn Asp Met Asp Val Thr Asn Ile Asp Tyr Thr Ser  
 130 135 140

Lys Thr Gly Asp Thr Ile Tyr Asn Gly Ile Ser Glu Leu Lys Asn Tyr  
 145 150 155 160

Thr Gly Ser Thr Gln Lys Met Lys Thr Asp Ser Phe Gln Arg Asp Tyr

38-21(52806) Sequence Listing\_PCT\_2.ST25.txt  
165 170 175Thr Lys Ser Glu Ser Thr Ser Val Thr Asn Gly Leu Gln Leu Gly Phe  
180 185 190Lys Val Ala Ala Lys Gly Val Val Ala Leu Ala Gly Ala Asp Phe Glu  
195 200 205Thr Ser Val Thr Tyr Asn Leu Ser Thr Thr Thr Glu Thr Asn Thr  
210 215 220Ile Ser Asp Lys Phe Thr Val Pro Ser Gln Glu Val Thr Leu Pro Pro  
225 230 235 240Gly His Lys Ala Ile Val Lys His Asp Leu Arg Lys Met Val Tyr Ser  
245 250 255Gly Thr His Asp Leu Lys Gly Asp Leu Ile Val Ser Phe Asn Asp Lys  
260 265 270Glu Ile Val Gln Lys Phe Ile Tyr Pro Asn Tyr Arg Glu Ile Asn Leu  
275 280 285Ser Asp Ile Arg Glu Thr Met Ile Glu Ile Asp Glu Trp Asn His Val  
290 295 300Asn Pro Val Asn Phe Tyr Glu Leu Val Gly Val Lys Asn His Ile Lys  
305 310 315 320Asn Gly Glu Thr Leu Tyr Ile Asp Thr Pro Ala Lys Phe Met Phe Asn  
325 330 335Gly Ala Asn Pro Tyr Tyr Arg Ala Thr Phe Thr Glu Tyr Asp Gly Asn  
340 345 350Asn Asn Pro Val Gln Thr Lys Val Leu Ser Glu Asn Phe Lys Leu  
355 360 365

&lt;210&gt; 5

&lt;211&gt; 1621

&lt;212&gt; DNA

<213> *Bacillus thuringiensis*

&lt;220&gt;

38-21(52806) Sequence Listing\_PCT\_2.ST25.txt

<221> CDS

<222> (530)..(1621)

<223>

<400> 5  
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 tccaatgtgt gccttcttat atcaatcgca cgatataaat aacactattt cccttgaat  
 tttatataagg tttcatctaa tttcaagac atgtggtgtt tttgcgtttt cttcttccaa 120  
 atttgataaa tcaagctccc atattcatga atccagcgca taatgattgt gggatgaact  
 gaaacatcac gatagcttaa agcaaaacga caatagtagc ggacggctac cataataata 180  
 tcttgttga actgttccc tttaaaatat cacatttgat attctcctcg atgcttttt 240  
 tagagtgttag cttcatctag aacactttgc aatagaacca ttcccttgat atacaattaa 300  
 accacattta tccttcatgg aatgtttata tattaaagaa tataaaaaaaa catacgatgt 360  
 tataattaat ttgaaagcgt taacaaaaat gaatgatgga gggataatt atg aaa tac  
 Met Lys Tyr 420  
 1  
 aag ttt tca aaa gtc gtt aag tgt act tta cca gct tta atg att act 480  
 Lys Phe Ser Lys Val Val Lys Cys Thr Leu Pro Ala Leu Met Ile Thr 538  
 5 10 15  
 aca ttc gtt act cca agt atg gca gtt ttt gcc gca gaa acc aag tcg 586  
 Thr Phe Val Thr Pro Ser Met Ala Val Phe Ala Ala Glu Thr Lys Ser  
 20 25 30 35  
 cca aat cta aat gca tct caa caa gca ata act cca tat gct gaa tct 634  
 Pro Asn Leu Asn Ala Ser Gln Gln Ala Ile Thr Pro Tyr Ala Glu Ser  
 40 45 50  
 tat att gat act gtt caa gat aga atg aaa caa aga gat agg gaa tca 682  
 Tyr Ile Asp Thr Val Gln Asp Arg Met Lys Gln Arg Asp Arg Glu Ser  
 55 60 65  
 aaa cta act ggt aaa cca ata aat atg caa gaa caa ata ata gat gga 730  
 Lys Leu Thr Gly Lys Pro Ile Asn Met Gln Glu Gln Ile Ile Asp Gly  
 70 75 80  
 tgg ttt tta gct aga ttc tgg ata ttt aaa gat caa aat aac aat cat 778  
 Trp Phe Leu Ala Arg Phe Trp Ile Phe Lys Asp Gln Asn Asn Asn His  
 85 90 95  
 caa aca aat aga ttt ata tcc tgg ttt aaa gat aat ctt gct agt tcg 826  
 Gln Thr Asn Arg Phe Ile Ser Trp Phe Lys Asp Asn Leu Ala Ser Ser  
 100 105 110 115  
 aag ggg tat gac agt ata gca gaa caa atg ggc tta aaa ata gaa gca 874  
 Lys Gly Tyr Asp Ser Ile Ala Glu Gln Met Gly Leu Lys Ile Glu Ala  
 120 125 130  
 tta aat gat atg gat gta aca aat att gat tat aca tct aaa aca ggt 922  
 Leu Asn Asp Met Asp Val Thr Asn Ile Asp Tyr Thr Ser Lys Thr Gly  
 970

135 38-21(52806) Sequence Listing\_PCT\_2.ST25.txt  
 140 145

gat acc ata tat aat gga att tct gaa cta aca aat tat aca gga aca Asp Thr Ile Tyr Asn Gly Ile Ser Glu Leu Thr Asn Tyr Thr Gly Thr 150 155 160	1018
acc caa aaa atg aaa acc gat agt ttt caa aga gat tat aca aaa tct Thr Gln Lys Met Lys Thr Asp Ser Phe Gln Arg Asp Tyr Thr Lys Ser 165 170 175	1066
gaa tcc act tca gta aca aat ggg tta caa tta gga ttt aaa gtt gct Glu Ser Thr Ser Val Thr Asn Gly Leu Gln Leu Gly Phe Lys Val Ala 180 185 190 195	1114
gct aag gga gta gtt gca tta gca ggt gca gat ttt gaa aca aca agt gtt Ala Lys Gly Val Val Ala Leu Ala Gly Ala Asp Phe Glu Thr Ser Val 200 205 210	1162
acc tat aat tta tca tct act aca act gaa aca aat aca ata tcg gat Thr Tyr Asn Leu Ser Ser Thr Thr Thr Glu Thr Asn Thr Ile Ser Asp 215 220 225	1210
aag ttt act gtt cca tct caa gaa gtt aca tta tcc cca gga cat aaa Lys Phe Thr Val Pro Ser Gln Glu Val Thr Leu Ser Pro Gly His Lys 230 235 240	1258
gca gtg gtg aaa cat gat ttg aga aaa atg gtg tat ttt ggg act cat Ala Val Val Lys His Asp Leu Arg Lys Met Val Tyr Phe Gly Thr His 245 250 255	1306
gat tta aag ggt gat tta aaa gta ggt ttt aat gat aaa gag att gta Asp Leu Lys Gly Asp Leu Lys Val Gly Phe Asn Asp Lys Glu Ile Val 260 265 270 275	1354
caa aaa ttt att tat cca aat tat aga tca att gat tta tct gat att Gln Lys Phe Ile Tyr Pro Asn Tyr Arg Ser Ile Asp Leu Ser Asp Ile 280 285 290	1402
cgt aaa aca atg att gaa att gat aaa tgg aat cat gta aat acc att Arg Lys Thr Met Ile Glu Ile Asp Lys Trp Asn His Val Asn Thr Ile 295 300 305	1450
gac ttt tat caa tta gtt gga gtt aaa aat cat ata aaa aat ggt gat Asp Phe Tyr Gln Leu Val Gly Val Lys Asn His Ile Lys Asn Gly Asp 310 315 320	1498
act tta tat ata gat acc ccg gcc gaa ttt aca ttt aat gga gct aat Thr Leu Tyr Ile Asp Thr Pro Ala Glu Phe Thr Phe Asn Gly Ala Asn 325 330 335	1546
cca tat tat aga gca aca ttt aca gaa tac gac gag aac gga aat cct Pro Tyr Tyr Arg Ala Thr Phe Thr Glu Tyr Asp Glu Asn Gly Asn Pro 340 345 350 355	1594
gtt caa aca aag att tta agt gga aat Val Gln Thr Lys Ile Leu Ser Gly Asn 360	1621

&lt;210&gt; 6

&lt;211&gt; 364

## 38-21(52806) Sequence Listing\_PCT\_2.ST25.txt

&lt;212&gt; PRT

<213> *Bacillus thuringiensis*

&lt;400&gt; 6

Met Lys Tyr Lys Phe Ser Lys Val Val Lys Cys Thr Leu Pro Ala Leu  
1 5 10 15

Met Ile Thr Thr Phe Val Thr Pro Ser Met Ala Val Phe Ala Ala Glu  
20 25 30

Thr Lys Ser Pro Asn Leu Asn Ala Ser Gln Gln Ala Ile Thr Pro Tyr  
35 40 45

Ala Glu Ser Tyr Ile Asp Thr Val Gln Asp Arg Met Lys Gln Arg Asp  
50 55 60

Arg Glu Ser Lys Leu Thr Gly Lys Pro Ile Asn Met Gln Glu Gln Ile  
65 70 75 80

Ile Asp Gly Trp Phe Leu Ala Arg Phe Trp Ile Phe Lys Asp Gln Asn  
85 90 95

Asn Asn His Gln Thr Asn Arg Phe Ile Ser Trp Phe Lys Asp Asn Leu  
100 105 110

Ala Ser Ser Lys Gly Tyr Asp Ser Ile Ala Glu Gln Met Gly Leu Lys  
115 120 125

Ile Glu Ala Leu Asn Asp Met Asp Val Thr Asn Ile Asp Tyr Thr Ser  
130 135 140

Lys Thr Gly Asp Thr Ile Tyr Asn Gly Ile Ser Glu Leu Thr Asn Tyr  
145 150 155 160

Thr Gly Thr Thr Gln Lys Met Lys Thr Asp Ser Phe Gln Arg Asp Tyr  
165 170 175

Thr Lys Ser Glu Ser Thr Ser Val Thr Asn Gly Leu Gln Leu Gly Phe  
180 185 190

Lys Val Ala Ala Lys Gly Val Val Ala Leu Ala Gly Ala Asp Phe Glu  
195 200 205

Thr Ser Val Thr Tyr Asn Leu Ser Ser Thr Thr Thr Glu Thr Asn Thr  
210 215 220

## 38-21(52806) Sequence Listing\_PCT\_2.ST25.txt

Ile Ser Asp Lys Phe Thr Val Pro Ser Gln Glu Val Thr Leu Ser Pro  
225 230 235 240

Gly His Lys Ala Val Val Lys His Asp Leu Arg Lys Met Val Tyr Phe  
245 250 255

Gly Thr His Asp Leu Lys Gly Asp Leu Lys Val Gly Phe Asn Asp Lys  
260 265 270

Glu Ile Val Gln Lys Phe Ile Tyr Pro Asn Tyr Arg Ser Ile Asp Leu  
275 280 285

Ser Asp Ile Arg Lys Thr Met Ile Glu Ile Asp Lys Trp Asn His Val  
290 295 300

Asn Thr Ile Asp Phe Tyr Gln Leu Val Gly Val Lys Asn His Ile Lys  
305 310 315 320

Asn Gly Asp Thr Leu Tyr Ile Asp Thr Pro Ala Glu Phe Thr Phe Asn  
325 330 335

Gly Ala Asn Pro Tyr Tyr Arg Ala Thr Phe Thr Glu Tyr Asp Glu Asn  
340 345 350

Gly Asn Pro Val Gln Thr Lys Ile Leu Ser Gly Asn  
355 360

<210> 7

<211> 1552

<212> DNA

<213> *Bacillus thuringiensis*

<220>

<221> CDS

<222> (169)..(1272)

<223>

<400> 7  
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aaccatattt atccttaaat aaatgttcac atatttaaaa agaataaact accatgcggt 120  
gctagaatat aaatgagagc gctaacaaaa aataatggag ggataatc atg aaa tac 177

## 38-21(52806) Sequence Listing\_PCT\_2.ST25.txt

Met Lys Tyr  
1

aaa tca tca aaa gta gca ata tgt act tta tca gct tta atg ctt tca	225
Lys Ser Ser Lys Val Ala Ile Cys Thr Leu Ser Ala Leu Met Leu Ser	
5 10 15	
aca att ggt act tcg agt atg tcc act ttt gct gca gaa aca aca tta	273
Thr Ile Gly Thr Ser Ser Met Ser Thr Phe Ala Ala Glu Thr Thr Leu	
20 25 30 35	
cca ggt caa act ctt aag gaa caa tca ata acc cca cgt gca gaa tct	321
Pro Gly Gln Thr Leu Lys Glu Gln Ser Ile Thr Pro Arg Ala Glu Ser	
40 45 50	
tat att gat att gta caa gat aga atg aaa caa agg gat ata gaa tcg	369
Tyr Ile Asp Ile Val Gln Asp Arg Met Lys Gln Arg Asp Ile Glu Ser	
55 60 65	
aaa cgt act ggt aaa ccg att aat atg caa gaa caa ata ata gat gga	417
Lys Arg Thr Gly Lys Pro Ile Asn Met Gln Glu Gln Ile Ile Asp Gly	
70 75 80	
tgg ttt tta gca aga ttc tgg ata ttt aaa gat caa aat aat aac cat	465
Trp Phe Leu Ala Arg Phe Trp Ile Phe Lys Asp Gln Asn Asn Asn His	
85 90 95	
caa aca aat aga ttc ata aca tgg ttt aaa aat aat gtt gcc agc tca	513
Gln Thr Asn Arg Phe Ile Thr Trp Phe Lys Asn Asn Val Ala Ser Ser	
100 105 110 115	
aaa ggt tat gag ggt att gca gaa caa atg ggt ttg aaa ata gaa tcg	561
Lys Gly Tyr Glu Gly Ile Ala Glu Gln Met Gly Leu Lys Ile Glu Ser	
120 125 130	
atg agt gat atg aat gta tcg aat ata aat tat aca ggt aaa aag ggt	609
Met Ser Asp Met Asn Val Ser Asn Ile Asn Tyr Thr Gly Lys Lys Gly	
135 140 145	
gat act ata tat aat ggc gtt tcg gaa tta gaa aat aaa atg gga aca	657
Asp Thr Ile Tyr Asn Gly Val Ser Glu Leu Glu Asn Lys Met Gly Thr	
150 155 160	
cct caa aaa atg aaa tca gat agt ttt caa aga gat tat acc aaa tct	705
Pro Gln Lys Met Lys Ser Asp Ser Phe Gln Arg Asp Tyr Thr Lys Ser	
165 170 175	
caa tca acc tca gta aca aat ggg tta caa tta gga gtt aaa gtt tct	753
Gln Ser Thr Ser Val Thr Asn Gly Leu Gln Leu Gly Val Lys Val Ser	
180 185 190 195	
gcc aaa ggt acg gtt gtc tta gga gag gca agc ctt gaa aca agc gtt	801
Ala Lys Gly Thr Val Val Leu Gly Glu Ala Ser Leu Glu Thr Ser Val	
200 205 210	
act tat aat tta tcg tct act gca act gaa aca gat aca aca tcg gac	849
Thr Tyr Asn Leu Ser Ser Thr Ala Thr Glu Thr Asp Thr Thr Ser Asp	
215 220 225	
aag ttt act gtc cca tcc caa gaa gtt aca tta cca cca gga cat aaa	897
Lys Phe Thr Val Pro Ser Gln Glu Val Thr Leu Pro Pro Gly His Lys	
230 235 240	

38-21(52806) Sequence Listing\_PCT\_2.ST25.txt

gca gta att aag cat gat tta aga aaa atg gtg tat tct ggt acg cat	945
Ala Val Ile Lys His Asp Leu Arg Lys Met Val Tyr Ser Gly Thr His	
245 250 255	
gac tta aag ggg gat tta aaa gta gct ttt aac gat aaa gca att gta	993
Asp Leu Lys Gly Asp Leu Lys Val Ala Phe Asn Asp Lys Ala Ile Val	
260 265 270 275	
caa aaa ttt att tat cca aat tat aga tct ata aat tta tct gat att	1041
Gln Lys Phe Ile Tyr Pro Asn Tyr Arg Ser Ile Asn Leu Ser Asp Ile	
280 285 290	
cgt aaa aca atg aaa gaa att gat gaa tgg aat cat gta aaa ccc att	1089
Arg Lys Thr Met Lys Glu Ile Asp Glu Trp Asn His Val Lys Pro Ile	
295 300 305	
gat ttt tat caa ctg gtt gga ata aaa aat cat ata aaa aat ggg gat	1137
Asp Phe Tyr Gln Leu Val Gly Ile Lys Asn His Ile Lys Asn Gly Asp	
310 315 320	
acc tta tat ata gag act cca gct aaa ttt att ttt aat gga gct aat	1185
Thr Leu Tyr Ile Glu Thr Pro Ala Lys Phe Ile Phe Asn Gly Ala Asn	
325 330 335	
gta tat tat aga gca act ttt aca gaa tat gat aag gat gga aaa cct	1233
Val Tyr Tyr Arg Ala Thr Phe Thr Glu Tyr Asp Lys Asp Gly Lys Pro	
340 345 350 355	
gtt caa ttc aac aaa ttt tta agt gaa aat tac aag tta tagaggaagt	1282
Val Gln Phe Asn Lys Phe Leu Ser Glu Asn Tyr Lys Leu	
360 365	
aaagatgccg tagtgagatc gttcacagc tactgagtat tcaaataata cacggaaaa	1342
ttcaccttcc tggaggacg gatttacttt ttttacggag gaaacctgttt tatacatcaa	1402
aatgtttttt tatgaggttt gtgtattctt attttagcctt ggaacggAAC cattttgagt	1462
aagcttaatt tgacttggaa atgtatTTT attaccttat tacgtgaaca atggcctata	1522
aacgtgccac acaggaatgg gaggacgagt	1552

&lt;210&gt; 8

&lt;211&gt; 368

&lt;212&gt; PRT

<213> *Bacillus thuringiensis*

&lt;400&gt; 8

Met Lys Tyr Lys Ser Ser Lys Val Ala Ile Cys Thr Leu Ser Ala Leu	
1 5 10 15	

Met Leu Ser Thr Ile Gly Thr Ser Ser Met Ser Thr Phe Ala Ala Glu	
20 25 30	

38-21(52806) Sequence Listing\_PCT\_2.ST25.txt

Thr Thr Leu Pro Gly Gln Thr Leu Lys Glu Gln Ser Ile Thr Pro Arg  
35 40 45

Ala Glu Ser Tyr Ile Asp Ile Val Gln Asp Arg Met Lys Gln Arg Asp  
50 55 60

Ile Glu Ser Lys Arg Thr Gly Lys Pro Ile Asn Met Gln Glu Gln Ile  
65 70 75 80

Ile Asp Gly Trp Phe Leu Ala Arg Phe Trp Ile Phe Lys Asp Gln Asn  
85 90 95

Asn Asn His Gln Thr Asn Arg Phe Ile Thr Trp Phe Lys Asn Asn Val  
100 105 110

Ala Ser Ser Lys Gly Tyr Glu Gly Ile Ala Glu Gln Met Gly Leu Lys  
115 120 125

Ile Glu Ser Met Ser Asp Met Asn Val Ser Asn Ile Asn Tyr Thr Gly  
130 135 140

Lys Lys Gly Asp Thr Ile Tyr Asn Gly Val Ser Glu Leu Glu Asn Lys  
145 150 155 160

Met Gly Thr Pro Gln Lys Met Lys Ser Asp Ser Phe Gln Arg Asp Tyr  
165 170 175

Thr Lys Ser Gln Ser Thr Ser Val Thr Asn Gly Leu Gln Leu Gly Val  
180 185 190

Lys Val Ser Ala Lys Gly Thr Val Val Leu Gly Glu Ala Ser Leu Glu  
195 200 205

Thr Ser Val Thr Tyr Asn Leu Ser Ser Thr Ala Thr Glu Thr Asp Thr  
210 215 220

Thr Ser Asp Lys Phe Thr Val Pro Ser Gln Glu Val Thr Leu Pro Pro  
225 230 235 240

Gly His Lys Ala Val Ile Lys His Asp Leu Arg Lys Met Val Tyr Ser  
245 250 255

Gly Thr His Asp Leu Lys Gly Asp Leu Lys Val Ala Phe Asn Asp Lys  
260 265 270

Ala Ile Val Gln Lys Phe Ile Tyr Pro Asn Tyr Arg Ser Ile Asn Leu  
275 280 285

## 38-21(52806) Sequence Listing\_PCT\_2.ST25.txt

Ser Asp Ile Arg Lys Thr Met Lys Glu Ile Asp Glu Trp Asn His Val  
 290 295 300

Lys Pro Ile Asp Phe Tyr Gln Leu Val Gly Ile Lys Asn His Ile Lys  
 305 310 315 320

Asn Gly Asp Thr Leu Tyr Ile Glu Thr Pro Ala Lys Phe Ile Phe Asn  
 325 330 335

Gly Ala Asn Val Tyr Tyr Arg Ala Thr Phe Thr Glu Tyr Asp Lys Asp  
 340 345 350

Gly Lys Pro Val Gln Phe Asn Lys Phe Leu Ser Glu Asn Tyr Lys Leu  
 355 360 365

<210> 9

<211> 1378

<212> DNA

<213> *Bacillus thuringiensis*

<220>

<221> CDS

<222> (215)..(1306)

<223>

<400> 9  
 cagtggatag gaattttgttt tcgtgctagg tatcaattta atttgttctta taagataagt 60  
 gaagtacgt caaaaatgaat acttttgtgt attagatcaa taggtaaaat aataataaaat 120  
 tttatatttg aaccctaaaaa aattatttaa tcaaatcttt ttcactttaa aaacaaaata 180  
 tccagaaaaaa acaatagttt acggagggat aata atg aaa tac aag tca tca aaa 235  
 Met Lys Tyr Lys Ser Ser Lys  
 1 5  
 gta gca atg tgt aca tta tca gct tta atg ctt tcg aca atc gcc act 283  
 Val Ala Met Cys Thr Leu Ser Ala Leu Met Leu Ser Thr Ile Ala Thr  
 10 15 20  
 cca agt ata tct gtt ttc gct gca gaa aca act tcg tca cat gcg gtt 331  
 Pro Ser Ile Ser Val Phe Ala Ala Glu Thr Thr Ser Ser His Ala Val  
 25 30 35  
 act aat cag caa aca att acg cag cgt gca gaa tct tat att gat att 379  
 Thr Asn Gln Gln Thr Ile Thr Gln Arg Ala Glu Ser Tyr Ile Asp Ile  
 40 45 50 55

## 38-21(52806) Sequence Listing\_PCT\_2.ST25.txt

gtg cac aat aga atg aaa caa aga gat att gaa tca aaa atg aca ggt	427
Val His Asn Arg Met Lys Gln Arg Asp Ile Glu Ser Lys Met Thr Gly	
60 65 70	
aaa tcc att aat atg caa gaa caa ata att gat gga tgg ttt tta gct	475
Lys Ser Ile Asn Met Gln Glu Gln Ile Ile Asp Gly Trp Phe Leu Ala	
75 80 85	
aga ttt tgg ata ttt aag gat caa aat aat agt cac caa aca aat aga	523
Arg Phe Trp Ile Phe Lys Asp Gln Asn Asn Ser His Gln Thr Asn Arg	
90 95 100	
ttt att tca tgg ttt aag gat aat ttg gct agc cca gga ggg tat gat	571
Phe Ile Ser Trp Phe Lys Asp Asn Leu Ala Ser Pro Gly Gly Tyr Asp	
105 110 115	
agt atc gct gaa cag atg ggc cta aaa gta gca gca tta aat gat atg	619
Ser Ile Ala Glu Gln Met Gly Leu Lys Val Ala Ala Leu Asn Asp Met	
120 125 130 135	
gat ata tca aat gta aat tat act tct aag aca ggg gat act ata tat	667
Asp Ile Ser Asn Val Asn Tyr Thr Ser Lys Thr Gly Asp Thr Ile Tyr	
140 145 150	
aat ggt gtt tca gaa tta aaa aat atc aca gga aca act caa aaa atg	715
Asn Gly Val Ser Glu Leu Lys Asn Ile Thr Gly Thr Thr Gln Lys Met	
155 160 165	
aaa aca gat agt ttt caa aga gat tat aca aaa tcc cag tca act tca	763
Lys Thr Asp Ser Phe Gln Arg Asp Tyr Thr Lys Ser Gln Ser Thr Ser	
170 175 180	
atc acc aat gga tta caa tta gga ttt aaa gtt tca gct aaa gga ata	811
Ile Thr Asn Gly Leu Gln Leu Gly Phe Lys Val Ser Ala Lys Gly Ile	
185 190 195	
gtg gcc tta gcc ggt gcg gat ttt gaa gca agt gta aac tat aat tta	859
Val Ala Leu Ala Gly Ala Asp Phe Glu Ala Ser Val Asn Tyr Asn Leu	
200 205 210 215	
tcc act acc gca act gaa acc aat aca ata tct gat aaa ttt acc gtt	907
Ser Thr Thr Ala Thr Glu Thr Asn Thr Ile Ser Asp Lys Phe Thr Val	
220 225 230	
cct tca caa gaa gtc aca tta gcg cca gga cat aag gcg atc gta aaa	955
Pro Ser Gln Glu Val Thr Leu Ala Pro Gly His Lys Ala Ile Val Lys	
235 240 245	
cat agt ttg aag aaa atg gta tac tct gga acg cat gat tta aaa gga	1003
His Ser Leu Lys Lys Met Val Tyr Ser Gly Thr His Asp Leu Lys Gly	
250 255 260	
gat tta aca att act ttt aat gat aag gat tta gtt caa aaa ttt att	1051
Asp Leu Thr Ile Thr Phe Asn Asp Lys Asp Leu Val Gln Lys Phe Ile	
265 270 275	
tat cca aat tat aaa gct att gat tta tct aat att cgt aaa gca atg	1099
Tyr Pro Asn Tyr Lys Ala Ile Asp Leu Ser Asn Ile Arg Lys Ala Met	
280 285 290 295	
aca gaa att gat gaa tgg aat cat gta aaa cct acc gat ttc tat caa	1147
Thr Glu Ile Asp Glu Trp Asn His Val Lys Pro Thr Asp Phe Tyr Gln	

38-21(52806) Sequence Listing\_PCT\_2.ST25.txt  
 300 305 310

tta gtt ggg aat aaa aat tat ata aaa aac ggg gac act tta tac atc 1195  
 Leu Val Gly Asn Lys Asn Tyr Ile Lys Asn Gly Asp Thr Leu Tyr Ile  
 315 320 325

gaa aca cct gct aaa ttc act ttg aat gga ggc aac cct tat tat aca 1243  
 Glu Thr Pro Ala Lys Phe Thr Leu Asn Gly Gly Asn Pro Tyr Tyr Thr  
 330 335 340

gca acc ttt acg gaa tat gat gaa aat gga aat caa gtc aaa aca aag 1291  
 Ala Thr Phe Thr Glu Tyr Asp Glu Asn Gly Asn Gln Val Lys Thr Lys  
 345 350 355

cgt tta aat aac aaa taagttactt aaaggttaatt cattaacaat gtatccatta 1346  
 Arg Leu Asn Asn Lys  
 360

tataattaat ttataaaaaat aatgttttaa aa 1378

<210> 10

<211> 364

<212> PRT

<213> *Bacillus thuringiensis*

<400> 10

Met Lys Tyr Lys Ser Ser Lys Val Ala Met Cys Thr Leu Ser Ala Leu  
 1 5 10 15

Met Leu Ser Thr Ile Ala Thr Pro Ser Ile Ser Val Phe Ala Ala Glu  
 20 25 30

Thr Thr Ser Ser His Ala Val Thr Asn Gln Gln Thr Ile Thr Gln Arg  
 35 40 45

Ala Glu Ser Tyr Ile Asp Ile Val His Asn Arg Met Lys Gln Arg Asp  
 50 55 60

Ile Glu Ser Lys Met Thr Gly Lys Ser Ile Asn Met Gln Glu Gln Ile  
 65 70 75 80

Ile Asp Gly Trp Phe Leu Ala Arg Phe Trp Ile Phe Lys Asp Gln Asn  
 85 90 95

Asn Ser His Gln Thr Asn Arg Phe Ile Ser Trp Phe Lys Asp Asn Leu  
 100 105 110

Ala Ser Pro Gly Gly Tyr Asp Ser Ile Ala Glu Gln Met Gly Leu Lys  
 115 120 125

## 38-21(52806) Sequence Listing\_PCT\_2.ST25.txt

Val Ala Ala Leu Asn Asp Met Asp Ile Ser Asn Val Asn Tyr Thr Ser  
130 135 140

Lys Thr Gly Asp Thr Ile Tyr Asn Gly Val Ser Glu Leu Lys Asn Ile  
145 150 155 160

Thr Gly Thr Thr Gln Lys Met Lys Thr Asp Ser Phe Gln Arg Asp Tyr  
165 170 175

Thr Lys Ser Gln Ser Thr Ser Ile Thr Asn Gly Leu Gln Leu Gly Phe  
180 185 190

Lys Val Ser Ala Lys Gly Ile Val Ala Leu Ala Gly Ala Asp Phe Glu  
195 200 205

Ala Ser Val Asn Tyr Asn Leu Ser Thr Thr Ala Thr Glu Thr Asn Thr  
210 215 220

Ile Ser Asp Lys Phe Thr Val Pro Ser Gln Glu Val Thr Leu Ala Pro  
225 230 235 240

Gly His Lys Ala Ile Val Lys His Ser Leu Lys Lys Met Val Tyr Ser  
245 250 255

Gly Thr His Asp Leu Lys Gly Asp Leu Thr Ile Thr Phe Asn Asp Lys  
260 265 270

Asp Leu Val Gln Lys Phe Ile Tyr Pro Asn Tyr Lys Ala Ile Asp Leu  
275 280 285

Ser Asn Ile Arg Lys Ala Met Thr Glu Ile Asp Glu Trp Asn His Val  
290 295 300

Lys Pro Thr Asp Phe Tyr Gln Leu Val Gly Asn Lys Asn Tyr Ile Lys  
305 310 315 320

Asn Gly Asp Thr Leu Tyr Ile Glu Thr Pro Ala Lys Phe Thr Leu Asn  
325 330 335

Gly Gly Asn Pro Tyr Tyr Thr Ala Thr Phe Thr Glu Tyr Asp Glu Asn  
340 345 350

Gly Asn Gln Val Lys Thr Lys Arg Leu Asn Asn Lys  
355 360

## 38-21(52806) Sequence Listing\_PCT\_2.ST25.txt

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> probe sequence, or amplification primer sequence for use with primer as set forth in SEQ ID NO 12, corresponding to CDS as set forth in SEQ ID NO 3 from 438-458, biased toward codons preferred in *Bacillus* species genes containing A or T in 3rd position

<400> 11

aataataatc atcaaacwaa t

21

<210> 12

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> probe sequence, or amplification primer sequence for use with SEQ ID NO 11 corresponding to SEQ ID NO 3 from nucleotide position 978- 998, biased toward codons preferred in *Bacillus* species genes in which A or T is in 3rd position

<400> 12

attwggataw ataaaattttt g

21

<210> 13

<211> 1101

<212> DNA

<213> Artificial Sequence

<220>

<223> coding sequence preferred for use in monocot species encoding a Bt TIC901 amino acid sequence variant

<220>

<221> CDS

<222> (1)..(1101)

<223>

## 38-21(52806) Sequence Listing\_PCT\_2.ST25.txt

<400> 13  
atg aag aac cgc ttc agc aag gtc gcc ctc tgc acg gtg cct atc ctc 48  
Met Lys Asn Arg Phe Ser Lys Val Ala Leu Cys Thr Val Pro Ile Leu  
1 5 10 15

atg gtt tct acg ttc gcg tcc agc tcg atg tcc gcg ttc gca gcg gag 96  
Met Val Ser Thr Phe Ala Ser Ser Met Ser Ala Phe Ala Ala Glu  
20 25 30

gcc aaa agt cct gac ttg aac gtg tcc caa cag gtc ata ggc cct tac 144  
Ala Lys Ser Pro Asp Leu Asn Val Ser Gln Gln Val Ile Gly Pro Tyr  
35 40 45

gca gaa tct tac atc gac atc gtc cag gac aga atg aag cag aga gac 192  
Ala Glu Ser Tyr Ile Asp Ile Val Gln Asp Arg Met Lys Gln Arg Asp  
50 55 60

aaa gga tcc aaa ctc act ggc aaa ccc atc aac atg caa gag cag atc 240  
Lys Gly Ser Lys Leu Thr Gly Lys Pro Ile Asn Met Gln Glu Gln Ile  
65 70 75 80

atc gat ggg tgg ttt ctc gca cga ttc tgg att ttc aag gat cag aac 288  
Ile Asp Gly Trp Phe Leu Ala Arg Phe Trp Ile Phe Lys Asp Gln Asn  
85 90 95

aat aac cac cag aca aac agg ttc atc tca tgg ttt aag gat aac atc 336  
Asn Asn His Gln Thr Asn Arg Phe Ile Ser Trp Phe Lys Asp Asn Ile  
100 105 110

gcc tca tct aag gga tac aac tca ata gcc gaa cag atg ggc ctc aaa 384  
Ala Ser Ser Lys Gly Tyr Asn Ser Ile Ala Glu Gln Met Gly Leu Lys  
115 120 125

atc gaa gca gag aat gat atg gac gtg aca aat atc gac tac act agt 432  
Ile Glu Ala Glu Asn Asp Met Asp Val Thr Asn Ile Asp Tyr Thr Ser  
130 135 140

aag acc gga gac aca atc tac aac ggc att tcg gaa ctt aaa aac tat 480  
Lys Thr Gly Asp Thr Ile Tyr Asn Gly Ile Ser Glu Leu Lys Asn Tyr  
145 150 155 160

acg ggc agc acc cag aaa atg aag acc gat agc ttt caa agg gac tac 528  
Thr Gly Ser Thr Gln Lys Met Lys Thr Asp Ser Phe Gln Arg Asp Tyr  
165 170 175

aca aaa tcc gag tcg acc tcc gtg acc aat ggc ctc cag ctg ggc ttc 576  
Thr Lys Ser Glu Ser Thr Ser Val Thr Asn Gly Leu Gln Leu Gly Phe  
180 185 190

aag gtg gca gca aag ggc gtc gtc gct tta gcc ggc gca gac ttc gag 624  
Lys Val Ala Ala Lys Gly Val Val Ala Leu Ala Gly Ala Asp Phe Glu  
195 200 205

act tcg gtg acc tac aat ctg tct aca act acg act gag acg aac aca 672  
Thr Ser Val Thr Tyr Asn Leu Ser Thr Thr Thr Glu Thr Asn Thr  
210 215 220

att tcc gac aag ttt acg gtt ccg tct cag gag gtt acg ttc cct cca 720  
Ile Ser Asp Lys Phe Thr Val Pro Ser Gln Glu Val Thr Phe Pro Pro  
225 230 235 240

## 38-21(52806) Sequence Listing\_PCT\_2.ST25.txt

ggc cac aag gca atc gtc aag cac gac ctg agg aaa atg gtc tac agc	768
Gly His Lys Ala Ile Val Lys His Asp Leu Arg Lys Met Val Tyr Ser	
245 250 255	
ggc acc cat gat ctc aaa ggc gac ctc atc gtg tcg ttc aac gac aag	816
Gly Thr His Asp Leu Lys Gly Asp Leu Ile Val Ser Phe Asn Asp Lys	
260 265 270	
gag ata gtc cag aag ttc atc tac cca aat tac cgc gac atc aac ctc	864
Glu Ile Val Gln Lys Phe Ile Tyr Pro Asn Tyr Arg Asp Ile Asn Leu	
275 280 285	
agt gac atc cga gag acc atg atc gag atc gac gag tgg aac cac gtg	912
Ser Asp Ile Arg Glu Thr Met Ile Glu Ile Asp Glu Trp Asn His Val	
290 295 300	
aac cct gtc aat ttc tac gaa ctc gta gga gtt aag aac cac atc aag	960
Asn Pro Val Asn Phe Tyr Glu Leu Val Gly Val Lys Asn His Ile Lys	
305 310 315 320	
aac ggt gaa aca ttg tac atc gac acg ccg gct aag ttc atg ttc aac	1008
Asn Gly Glu Thr Leu Tyr Ile Asp Thr Pro Ala Lys Phe Met Phe Asn	
325 330 335	
gga gcg aat cct tac tat cga gct acc ttc acg gag tac gat ggc aac	1056
Gly Ala Asn Pro Tyr Tyr Arg Ala Thr Phe Thr Glu Tyr Asp Gly Asn	
340 345 350	
aac aat cct gtt cag acc aag gtg ttg agt gag aat ttc aag ctg	1101
Asn Asn Pro Val Gln Thr Lys Val Leu Ser Glu Asn Phe Lys Leu	
355 360 365	

&lt;210&gt; 14

&lt;211&gt; 367

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; coding sequence preferred for use in monocot species encoding a Bt TIC901 amino acid sequence variant

&lt;400&gt; 14

Met Lys Asn Arg Phe Ser Lys Val Ala Leu Cys Thr Val Pro Ile Leu	
1 5 10 15	

Met Val Ser Thr Phe Ala Ser Ser Met Ser Ala Phe Ala Ala Glu	
20 25 30	

Ala Lys Ser Pro Asp Leu Asn Val Ser Gln Gln Val Ile Gly Pro Tyr	
35 40 45	

38-21(52806) Sequence Listing\_PCT\_2.ST25.txt

Ala Glu Ser Tyr Ile Asp Ile Val Gln Asp Arg Met Lys Gln Arg Asp  
50 55 60

Lys Gly Ser Lys Leu Thr Gly Lys Pro Ile Asn Met Gln Glu Gln Ile  
65 70 75 80

Ile Asp Gly Trp Phe Leu Ala Arg Phe Trp Ile Phe Lys Asp Gln Asn  
85 90 95

Asn Asn His Gln Thr Asn Arg Phe Ile Ser Trp Phe Lys Asp Asn Ile  
100 105 110

Ala Ser Ser Lys Gly Tyr Asn Ser Ile Ala Glu Gln Met Gly Leu Lys  
115 120 125

Ile Glu Ala Glu Asn Asp Met Asp Val Thr Asn Ile Asp Tyr Thr Ser  
130 135 140

Lys Thr Gly Asp Thr Ile Tyr Asn Gly Ile Ser Glu Leu Lys Asn Tyr  
145 150 155 160

Thr Gly Ser Thr Gln Lys Met Lys Thr Asp Ser Phe Gln Arg Asp Tyr  
165 170 175

Thr Lys Ser Glu Ser Thr Ser Val Thr Asn Gly Leu Gln Leu Gly Phe  
180 185 190

Lys Val Ala Ala Lys Gly Val Val Ala Leu Ala Gly Ala Asp Phe Glu  
195 200 205

Thr Ser Val Thr Tyr Asn Leu Ser Thr Thr Thr Glu Thr Asn Thr  
210 215 220

Ile Ser Asp Lys Phe Thr Val Pro Ser Gln Glu Val Thr Phe Pro Pro  
225 230 235 240

Gly His Lys Ala Ile Val Lys His Asp Leu Arg Lys Met Val Tyr Ser  
245 250 255

Gly Thr His Asp Leu Lys Gly Asp Leu Ile Val Ser Phe Asn Asp Lys  
260 265 270

Glu Ile Val Gln Lys Phe Ile Tyr Pro Asn Tyr Arg Asp Ile Asn Leu  
275 280 285

Ser Asp Ile Arg Glu Thr Met Ile Glu Ile Asp Glu Trp Asn His Val  
290 295 300

## 38-21(52806) Sequence Listing\_PCT\_2.ST25.txt

Asn Pro Val Asn Phe Tyr Glu Leu Val Gly Val Lys Asn His Ile Lys  
305 310 315 320

Asn Gly Glu Thr Leu Tyr Ile Asp Thr Pro Ala Lys Phe Met Phe Asn  
325 330 335

Gly Ala Asn Pro Tyr Tyr Arg Ala Thr Phe Thr Glu Tyr Asp Gly Asn  
340 345 350

Asn Asn Pro Val Gln Thr Lys Val Leu Ser Glu Asn Phe Lys Leu  
355 360 365

<210> 15

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide primer coupled with prJPW152 SEQ ID NO 16 in thermal amplification reactions

<400> 15

cctttggcag aaactttaac tcc 23

<210> 16

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide primer coupled with prJPW151 SEQ ID NO 15 in thermal amplification reactions

<400> 16

gtgttattctg gtacgcatga c 21

<210> 17

<211> 34

<212> DNA

<213> Artificial Sequence

## 38-21(52806) Sequence Listing\_PCT\_2.ST25.txt

&lt;220&gt;

&lt;223&gt; oligonucleotide primer coupled with prJPW183 SEQ ID NO 18 in thermal amplification reactions

<400> 17  
gccggatccc tagctgaata tgcagtagat aatg 34

&lt;210&gt; 18

&lt;211&gt; 25

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; oligonucleotide primer coupled with prJPW186 SEQ ID NO 17 in thermal amplification reactions

<400> 18  
gtggcacgtt tataggccat tgttc 25

&lt;210&gt; 19

&lt;211&gt; 23

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; oligonucleotide primer coupled with prJPW156 SEQ ID NO 20 in thermal amplification reactions

<400> 19  
cttttaggcc catctgttca gcg 23

&lt;210&gt; 20

&lt;211&gt; 26

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; oligonucleotide primer coupled with prJPW155 SEQ ID NO 19 in thermal amplification reactions

38-21(52806) Sequence Listing\_PCT\_2.ST25.txt

<400> 20  
gccttagccg gtgcggattt tgaagg

<210> 21

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide primer coupled with prJPW170 SEQ ID NO 22 in thermal amplification reactions

<400> 21  
ggagcttattttaa acgctttgtt ttgacttgat ttcc 44

<210> 22

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide primer coupled with prJPW168 SEQ ID NO 21 in thermal amplification reactions

<400> 22  
gccggatccc agtggatagg aatttgtttt cgtgctagg 39

<210> 23

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> universal forward amplification primer similar to SEQ ID NO:24 and SEQ ID NO:25 that, when used in a thermal amplification reaction with any of SEQ ID NO:SEQ ID NO:27-29 and template DNA homologous to tic901, 1201, 407, 417, or 431 and the like result in amplicon of from about 600 to about 650 base pairs

<400> 23  
aayatgcarg arcarathat hgaygg 23

## 38-21(52806) Sequence Listing\_PCT\_2.ST25.txt

<210> 24

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> universal forward amplification primer similar to SEQ ID NO:23 and SEQ ID NO:25 that, when used in a thermal amplification reaction with any of SEQ ID NO:27-29 and template DNA homologous to tic901, 1201, 407, 417, or 431 and the like result in amplicon of from about 600 to about 650 base pairs

<400> 24

aayatgcarg arcarathat hga

23

<210> 25

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> universal forward amplification primer similar to SEQ ID NO:23 and SEQ ID NO:24 that, when used in a thermal amplification reaction with any of SEQ ID NO:27-29 and template DNA homologous to tic901, 1201, 407, 417, or 431 and the like result in amplicon of from about 600 to about 650 base pairs

<400> 25

aayatgcarg arcarathat

20

<210> 26

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> universal forward amplification primer that, when used in a thermal amplification reaction with any of SEQ ID NO:27-29 and template DNA homologous to tic901, 1201, 407, 417, 431 and the like result in amplicon of from about 395 to about 425 base pairs

## 38-21(52806) Sequence Listing\_PCT\_2.ST25.txt

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (3)..(3)

&lt;223&gt; inosine

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (9)..(9)

&lt;223&gt; inosine

&lt;400&gt; 26

ggngayacna thtayaaygg

20

&lt;210&gt; 27

&lt;211&gt; 26

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; universal reverse amplification primer similar to SEQ ID NO:28 and SEQ ID NO:29

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (6)..(6)

&lt;223&gt; inosine

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (24)..(24)

&lt;223&gt; inosine

&lt;400&gt; 27

tarttnggrt adatraaytt ytgnac

26

## 38-21(52806) Sequence Listing\_PCT\_2.ST25.txt

&lt;210&gt; 28

&lt;211&gt; 23

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; universal reverse amplification primer similar to SEQ ID NO:27 and SEQ ID NO:29

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (6)..(6)

&lt;223&gt; inosine

&lt;400&gt; 28

tarttnggrt adatraaytt ytg

23

&lt;210&gt; 29

&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; universal reverse amplification primer similar to SEQ ID NO:27 and SEQ ID NO:28

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (18)..(18)

&lt;223&gt; inosine

&lt;400&gt; 29

ggrtadatra aytttytgnac

20

&lt;210&gt; 30

&lt;211&gt; 570

&lt;212&gt; DNA

38-21(52806) Sequence Listing\_PCT\_2.ST25.txt

<213> *Bacillus thuringiensis*

<220>

<221> CDS

<222> (1)..(570)

<223>

## 38-21(52806) Sequence Listing\_PCT\_2.ST25.txt

&lt;210&gt; 31

&lt;211&gt; 190

&lt;212&gt; PRT

<213> *Bacillus thuringiensis*

&lt;400&gt; 31

Phe Leu Ala Arg Phe Trp Ile Phe Glu Asp Gln Asn Asn Ser His Gln  
1 5 10 15

Thr Asn Arg Phe Ile Ser Trp Phe Lys Asp Asn Ile Ala Ser Ser Lys  
20 25 30

Gly Tyr Asn Ser Ile Ala Glu Gln Met Gly Leu Lys Ile Glu Ala Glu  
35 40 45

Asn Asp Met Asp Val Thr Asn Ile Asp Tyr Thr Ser Lys Thr Gly Asp  
50 55 60

Thr Ile Tyr Asn Gly Ile Ser Glu Leu Lys Asn Tyr Thr Gly Ser Thr  
65 70 75 80

Gln Lys Met Lys Thr Asp Ser Phe Gln Arg Asp Tyr Thr Lys Ser Glu  
85 90 95

Ser Thr Ser Val Thr Asn Gly Leu Gln Leu Gly Phe Lys Val Ala Ala  
100 105 110

Lys Gly Val Val Ala Leu Ala Gly Ala Asp Phe Glu Thr Ser Val Thr  
115 120 125

Tyr Asn Leu Ser Thr Thr Thr Glu Thr Asn Thr Ile Ser Asp Lys  
130 135 140

Phe Thr Val Pro Ser Gln Glu Val Thr Leu Pro Pro Gly His Lys Ala  
145 150 155 160

Ile Val Lys His Asp Leu Arg Lys Met Val Tyr Ser Gly Thr His Asp  
165 170 175

Leu Lys Gly Asp Leu Ile Val Ser Phe Asn Asp Lys Glu Ile  
180 185 190

&lt;210&gt; 32

## 38-21(52806) Sequence Listing\_PCT\_2.ST25.txt

&lt;211&gt; 1095

&lt;212&gt; DNA

<213> *Bacillus thuringiensis*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1092)

&lt;223&gt; sequence encoding TIC431 precursor amino acid sequence

<400> 32		
atg aaa tac aag tct tca aaa gta gca atg tgt aca tta tcg gct tta		48
Met Lys Tyr Lys Ser Ser Lys Val Ala Met Cys Thr Leu Ser Ala Leu		
1 5 10 15		
atg ctt tcg aca atc gcc act cca agt ata tct gtt ttc gct gct gaa		96
Met Leu Ser Thr Ile Ala Thr Pro Ser Ile Ser Val Phe Ala Ala Glu		
20 25 30		
aca act gca tca cat aag gtt act aat cag caa aca att gca cag cgt		144
Thr Thr Ala Ser His Lys Val Thr Asn Gln Gln Thr Ile Ala Gln Arg		
35 40 45		
gca gaa tct tat atc gat att gtg cat aat aga atg aaa aaa cga gat		192
Ala Glu Ser Tyr Ile Asp Ile Val His Asn Arg Met Lys Lys Arg Asp		
50 55 60		
att gaa tca aaa atg aca ggt aaa cct att aat atg caa gaa caa ata		240
Ile Glu Ser Lys Met Thr Gly Lys Pro Ile Asn Met Gln Glu Gln Ile		
65 70 75 80		
att gat gga tgg ttt tta gct aga ttt tgg ata ttc aag gac caa aat		288
Ile Asp Gly Trp Phe Leu Ala Arg Phe Trp Ile Phe Lys Asp Gln Asn		
85 90 95		
aat agt cac caa aca aat aga ttt att tca tgg ttt aaa gat aat tta		336
Asn Ser His Gln Thr Asn Arg Phe Ile Ser Trp Phe Lys Asp Asn Leu		
100 105 110		
gct agt cca gga ggg tat aat agt atc gct aaa caa atg ggg tta aaa		384
Ala Ser Pro Gly Gly Tyr Asn Ser Ile Ala Lys Gln Met Gly Leu Lys		
115 120 125		
ata gaa gta tta aat gat atg gat ata tca aat gta aat tat act tct		432
Ile Glu Val Leu Asn Asp Met Asp Ile Ser Asn Val Asn Tyr Thr Ser		
130 135 140		
aag aca ggg gat act ata tat aat ggt gtt tcc gaa tta aaa aat atc		480
Lys Thr Gly Asp Thr Ile Tyr Asn Gly Val Ser Glu Leu Lys Asn Ile		
145 150 155 160		
aca ggt aca act caa aaa atg aaa aca gat agt ttt caa aga gat tat		528
Thr Gly Thr Thr Gln Lys Met Lys Thr Asp Ser Phe Gln Arg Asp Tyr		
165 170 175		

## 38-21(52806) Sequence Listing\_PCT\_2.ST25.txt

aca aaa tca cag tca act tca atc acc aat gga tta caa tta gga ttt	576
Thr Lys Ser Gln Ser Thr Ser Ile Thr Asn Gly Leu Gln Leu Gly Phe	
180 185 190	
aaa gtt tct gcc aaa ggg gtg ata gct tta gca gga gca gac ttc gaa	624
Lys Val Ser Ala Lys Gly Val Ile Ala Leu Ala Gly Ala Asp Phe Glu	
195 200 205	
gca agt gtc aac tat aat tta tcc act acc gca act gaa acc aat ata	672
Ala Ser Val Asn Tyr Asn Leu Ser Thr Thr Ala Thr Glu Thr Asn Ile	
210 215 220	
ata tct gat aaa ttt acc gtt cct tca caa gaa gtt aca tta gcg cca	720
Ile Ser Asp Lys Phe Thr Val Pro Ser Gln Glu Val Thr Leu Ala Pro	
225 230 235 240	
gga cat aag gcg atc gta aaa cat agt tta aag aaa atg gta tac tcc	768
Gly His Lys Ala Ile Val Lys His Ser Leu Lys Lys Met Val Tyr Ser	
245 250 255	
gga acg cat gat tta aaa gga gat tta aca att act ttt aat gat aag	816
Gly Thr His Asp Leu Lys Gly Asp Leu Thr Ile Thr Phe Asn Asp Lys	
260 265 270	
gat tta gtt caa aaa ttt att tat cca aat tat aaa gct att gat tta	864
Asp Leu Val Gln Lys Phe Ile Tyr Pro Asn Tyr Lys Ala Ile Asp Leu	
275 280 285	
tct aat att cgt aaa gca ctg act gaa att gat gaa tgg aat cat gta	912
Ser Asn Ile Arg Lys Ala Leu Thr Glu Ile Asp Glu Trp Asn His Val	
290 295 300	
aaa cct acc gat ttc tat caa tta gtt ggg aac aaa aat tat ata aaa	960
Lys Pro Thr Asp Phe Tyr Gln Leu Val Gly Asn Lys Asn Tyr Ile Lys	
305 310 315 320	
aac ggg gac act tta tac atc gaa aca cct gct aaa ttc act ttg aat	1008
Asn Gly Asp Thr Leu Tyr Ile Glu Thr Pro Ala Lys Phe Thr Leu Asn	
325 330 335	
gga gga aac cct tat tat aca gca acc ttt acg gaa tat gat gaa agt	1056
Gly Gly Asn Pro Tyr Tyr Thr Ala Thr Phe Thr Glu Tyr Asp Glu Ser	
340 345 350	
gga aat caa gtc aaa aca aag cat tta agt gtc aaa taa	1095
Gly Asn Gln Val Lys Thr Lys His Leu Ser Val Lys	
355 360	

&lt;210&gt; 33

&lt;211&gt; 364

&lt;212&gt; PRT

<213> *Bacillus thuringiensis*

&lt;400&gt; 33

Met Lys Tyr Lys Ser Ser Lys Val Ala Met Cys Thr Leu Ser Ala Leu

1 5 38-21(52806) Sequence Listing\_PCT\_2.ST25.txt  
10 15Met Leu Ser Thr Ile Ala Thr Pro Ser Ile Ser Val Phe Ala Ala Glu  
20 25 30Thr Thr Ala Ser His Lys Val Thr Asn Gln Gln Thr Ile Ala Gln Arg  
35 40 45Ala Glu Ser Tyr Ile Asp Ile Val His Asn Arg Met Lys Lys Arg Asp  
50 55 60Ile Glu Ser Lys Met Thr Gly Lys Pro Ile Asn Met Gln Glu Gln Ile  
65 70 75 80Ile Asp Gly Trp Phe Leu Ala Arg Phe Trp Ile Phe Lys Asp Gln Asn  
85 90 95Asn Ser His Gln Thr Asn Arg Phe Ile Ser Trp Phe Lys Asp Asn Leu  
100 105 110Ala Ser Pro Gly Gly Tyr Asn Ser Ile Ala Lys Gln Met Gly Leu Lys  
115 120 125Ile Glu Val Leu Asn Asp Met Asp Ile Ser Asn Val Asn Tyr Thr Ser  
130 135 140Lys Thr Gly Asp Thr Ile Tyr Asn Gly Val Ser Glu Leu Lys Asn Ile  
145 150 155 160Thr Gly Thr Thr Gln Lys Met Lys Thr Asp Ser Phe Gln Arg Asp Tyr  
165 170 175Thr Lys Ser Gln Ser Thr Ser Ile Thr Asn Gly Leu Gln Leu Gly Phe  
180 185 190Lys Val Ser Ala Lys Gly Val Ile Ala Leu Ala Gly Ala Asp Phe Glu  
195 200 205Ala Ser Val Asn Tyr Asn Leu Ser Thr Thr Ala Thr Glu Thr Asn Ile  
210 215 220Ile Ser Asp Lys Phe Thr Val Pro Ser Gln Glu Val Thr Leu Ala Pro  
225 230 235 240Gly His Lys Ala Ile Val Lys His Ser Leu Lys Lys Met Val Tyr Ser  
245 250 255

38-21(52806) Sequence Listing\_PCT\_2.ST25.txt  
Gly Thr His Asp Leu Lys Gly Asp Leu Thr Ile Thr Phe Asn Asp Lys  
260 265 270

Asp Leu Val Gln Lys Phe Ile Tyr Pro Asn Tyr Lys Ala Ile Asp Leu  
275 280 285

Ser Asn Ile Arg Lys Ala Leu Thr Glu Ile Asp Glu Trp Asn His Val  
290 295 300

Lys Pro Thr Asp Phe Tyr Gln Leu Val Gly Asn Lys Asn Tyr Ile Lys  
305 310 315 320

Asn Gly Asp Thr Leu Tyr Ile Glu Thr Pro Ala Lys Phe Thr Leu Asn  
325 330 335

Gly Gly Asn Pro Tyr Tyr Thr Ala Thr Phe Thr Glu Tyr Asp Glu Ser  
340 345 350

Gly Asn Gln Val Lys Thr Lys His Leu Ser Val Lys  
355 360